

## SEARCH REQUEST FORM

6-445

Requestor's Name: Kaufman - Rm 10E07 Serial Number: 08/878,168  
 Date: 6/12/98 Phone: 305-5791 Art Unit: 1646

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search SEQ ID NO:1-4

• Fragment of SEQ ID NO:1 from amino acid 1-161, ~~all~~

in commercial, issued & pending patent databases.

Please put results on disk.

Thanks,  
Claire

SEARCHED 12 JUN 1998

## STAFF USE ONLY

Date completed: 6-22-98  
 Searcher: mk  
 Terminal time: 12  
 Elapsed time: 105  
 CPU time:  
 Total time: 15  
 Number of Searches: 1  
 Number of Databases: 1

Search Site	Vendors
<input checked="" type="checkbox"/> STIC	<u>MS 52 C6</u> <u>IG-Suite</u>
<input checked="" type="checkbox"/> CM-1	<u>STN</u>
<input checked="" type="checkbox"/> Pre-S	<u>Dialog</u>
<b>Type of Search</b>	
<input checked="" type="checkbox"/> N.A. Sequence	<u>APS</u>
<input checked="" type="checkbox"/> A.A. Sequence	<u>Geninfo</u>
<input checked="" type="checkbox"/> Structure	<u>SDC</u>
<input checked="" type="checkbox"/> Bibliographic	<u>DARC/Questel</u> <u>Other</u>

RESULT 1: Comparison to SEQ ID NO:4 (Qy)  
 LOCUS AF012536 1180 bp mRNA PRI 21-AUG-1997  
 DEFINITION Homo sapiens decoy receptor 1 (DcR1) mRNA, complete cds.  
 ACCESSION AF012536  
 NID g2338421  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
     Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
     Homo.  
 REFERENCE 1 (bases 1 to 1180)  
 AUTHORS Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Skubatch,M.,  
     Baldwin,D., Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I.,  
     Goddard,A.D., Godowski,P. and Ashkenazi,A.  
 TITLE Control of TRAIL-induced apoptosis by a family of signaling and  
     decoy receptors *ext.Aug. 8*  
 JOURNAL Science 277 (5327), 818-821 (1997) 0  
 MEDLINE 97390509  
 REFERENCE 2 (bases 1 to 1180)  
 AUTHORS Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Baldwin,D.,  
     Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I., Goddard,A.D.,  
     Godowski,P. and Ashkenazi,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1997) Molecular Oncology, Genentech, 1 DNA Way,  
     South San Francisco, CA 94080, USA  
 FEATURES Location/Qualifiers  
 source 1. .1180  
     /organism="Homo sapiens"  
     /db\_xref="taxon:9606"  
 gene 1. .1180  
     /gene="DcR1"  
 CDS 193. .972  
     /gene="DcR1"  
     /note="tumor necrosis factor receptor family member;  
     inhibits apoptosis induction by TRAIL/Apo2L"  
     /codon\_start=1  
     /product="decoy receptor 1"  
     /db\_xref="PID:g2338422"  
     /translation="MARIPKTLKFVVVIVAVLLPVILAYSATTARQEEVPQQTVAPQQQ  
     RHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQHKSSCT  
     MTRDTVCQCKEGTFRNENSPEMCRKCSRPSGEVQVSNCTS WDDIQCVEFGANATVE  
     TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTSPGTPAPAAEETMTSPG  
     TPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV"  
 BASE COUNT 338 a 326 c 298 g 218 t  
 ORIGIN

Query Match 100.0%; Score 1180; DB 22; Length 1180;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 1180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1 GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGA	60
Qy	1 GCTGTGGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGA	60

Db 61 GTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTCCTACCGTTAGGAACTCTGGGAC 120  
Qy 61 ||||||| GTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTCCTACCGTTAGGAACTCTGGGAC 120

Db 121 AGAGCGCCCCGGCGCCTGATGGCCGAGGCAGGGTGCAGCCAGGACCCAGGACGGCGTC 180  
Qy 121 AGAGCGCCCCGGCGCCTGATGGCCGAGGCAGGGTGCAGCCAGGACCCAGGACGGCGTC 180

Db 181 GGGAACCATACCATGGCCCGGATCCCCAAGACCTAAAGTCGTCGTCATCGTCGCG 240  
Qy 181 GGGAACCATACCATGGCCCGGATCCCCAAGACCTAAAGTCGTCGTCATCGTCGCG 240

Db 241 GTCCTGCTGCCAGTCCTAGCTTACTCTGCCACCCTGCCGGCAGGAGGAAGTTCCCCAG 300  
Qy 241 GTCCTGCTGCCAGTCCTAGCTTACTCTGCCACCCTGCCGGCAGGAGGAAGTTCCCCAG 300

Db 301 CAGACAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGA 360  
Qy 301 CAGACAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGA 360

Db 361 TCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACC 420  
Qy 361 TCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACC 420

Db 421 AACGCTTCCAACAATGAACCTTCTTGCTTCCCAGTACAGTTGTAAATCAGATCAAAAAA 480  
Qy 421 AACGCTTCCAACAATGAACCTTCTTGCTTCCCAGTACAGTTGTAAATCAGATCAAAAAA 480

Db 481 CATAAAAGTTCCCTGCACCATGACCAGAGACACAGTGTGTCAAGGGCACCTTC 540  
Qy 481 CATAAAAGTTCCCTGCACCATGACCAGAGACACAGTGTGTCAAGGGCACCTTC 540

Db 541 CGGAATGAAAACCTCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTC 600  
Qy 541 CGGAATGAAAACCTCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTC 600

Db 601 CAAGTCAGTAATTGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAAT 660  
Qy 601 CAAGTCAGTAATTGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAAT 660

Db 661 GCCACTGTGGAAACCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCC 720  
Qy 661 GCCACTGTGGAAACCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCC 720

Db 721 CCAGCTGCTGAAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAG 780  
Qy 721 CCAGCTGCTGAAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAG 780

Db 781 ACAATGACCACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCGC 840  
Qy 781 ACAATGACCACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCGC 840

Db 841 CCGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCGCCGGGACTCCTGCC 900  
Qy 841 CCGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCGCCGGGACTCCTGCC 900

Db 901 TCTTCTCATTACCTCTCATGCACCACATCGTAGGGATCATAGTTCTAATTGTGCTTGATT 960  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 901 TCTTCTCATTACCTCTCATGCACCACATCGTAGGGATCATAGTTCTAATTGTGCTTGATT 960

Db 961 GTGTTGTTGAAAGACTTCACTGTGGAAGAAATTCCCTCCTTACCTGAAAGGTTCAAGGT 1020  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 961 GTGTTGTTGAAAGACTTCACTGTGGAAGAAATTCCCTCCTTACCTGAAAGGTTCAAGGT 1020

Db 1021 AGGCCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTTGCTGTGT 1080  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1021 AGGCCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTTGCTGTGT 1080

Db 1081 TCCCACAGACAGAAACGCCTGCCCTGCCCAAAAAAAAAAAAAAAA 1140  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1081 TCCCACAGACAGAAACGCCTGCCCTGCCCAAAAAAAAAAAAAAAA 1140

Db 1141 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1180  
||| ||| ||| ||| ||| ||| ||| |||  
Qy 1141 AAAAAAAAAAAAAAAAAAAAAAAA 1180

RESULT 3: Comparison to SEQ ID NO:4 (Qy)  
 LOCUS AF016267 1388 bp mRNA PRI 16-OCT-1997  
 DEFINITION Homo sapiens TRAIL receptor 3 mRNA, complete cds.  
 ACCESSION AF016267  
 NID g2529564  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
     Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
     Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1388)  
 AUTHORS Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and Tschopp,J.  
 TITLE Characterization of two receptors binding TRAIL  
 JOURNAL FEBS Lett. (1997) In press  
 REFERENCE 2 (bases 1 to 1388)  
 AUTHORS Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and Tschopp,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUL-1997) Institute of Biochemistry, University of Lausanne, Chemin des Boveresses 155, Epalinges, VD 1066, Switzerland  
 FEATURES Location/Qualifiers  
 source 1. 1388  
     /organism="Homo sapiens"  
     /db\_xref="taxon:9606"  
     /dev\_stage="fetal"  
     /tissue\_type="liver and spleen"  
 CDS 188. 967  
     /function="binds cytotoxic ligand TRAIL"  
     /note="DR4 homolog; contains no intracellular domain"  
     /codon\_start=1  
     /product="TRAIL receptor 3"  
     /db\_xref="PID:g2529565"  
     /translation="MARIPKTLKFVVVIVAVLLPVLAGSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTRDTVCQCKEGTFRNVNSPEMCRKCSRCPSGEVQVSNCNTSWDDIQCVEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTASSHYLSCTIVGIIVLIVLLIVFV"  
 BASE COUNT 331 a 415 c 368 g 274 t  
 ORIGIN  
 Query Match 92.0%; Score 1086; DB 22; Length 1388;  
 Best Local Similarity 99.7%; Pred. No. 0.00e+00;  
 Matches 1094; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 Db 13 CACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGAGTTGACCAGAGATGC 72  
     |||||||  
 Qy 17 CACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGAGTTGACCAGAGATGC 76  
 Db 73 AAGGGGTGAAGGAGCGCTCCTACCGTTAGG-AACTCTGGGGACAGAGCGCCCCGGCCGC 131  
     |||||||  
 Qy 77 AAGGGGTGAAGGAGCGCTCCTACCGTTAGGAACTCTGGGGACAGAGCGCCCCGGCCGC 136  
 Db 132 CTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGAACCATACCATGG 191

Qy 137 ||||||| CTGATGGCGAGGCAGGGTGCACCCAGGACCCAGGACGGCTCGGTGGAAACCATAACATGG 196  
Db 192 CCCGGATCCCCAAGACCCCTAAAGTCGTCGTCATCGTCGCGTCCTGCTGCCAGTCC 251  
Qy 197 CCCGGATCCCCAAGACCCCTAAAGTCGTCGTCATCGTCGCGTCCTGCTGCCAGTCC 256  
Db 252 TAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCAC 311  
Qy 257 TAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTTCCCCAGCAGACAGTGGCCCCAC 316  
Db 312 AGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 371  
Qy 317 AGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 376  
Db 372 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCAAACAATG 431  
Qy 377 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCAAACAATG 436  
Db 432 AACCTTCTTGCTTCCCATGTACAGTTGTAAATCAGATCAAAAACATAAAAGTTCCCTGCA 491  
Qy 437 AACCTTCTTGCTTCCCATGTACAGTTGTAAATCAGATCAAAAACATAAAAGTTCCCTGCA 496  
Db 492 CCATGACCAGAGACACAGTGTGCAGTGTAAAGAAGGCACCTTCCGGAATGTTAACTCCC 551  
Qy 497 CCATGACCAGAGACACAGTGTGCAGTGTAAAGAAGGCACCTTCCGGAATGAAAACCTCCC 556  
Db 552 CAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAATTGTA 611  
Qy 557 CAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAATTGTA 616  
Db 612 CGTCCTGGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAAACCC 671  
Qy 617 CGTCCTGGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAAACCC 676  
Db 672 CAGCTGCTGAAGAGACAATGAACACCAAGCCGGGACTCCTGCCAGCTGCTGAAGAGA 731  
Qy 677 CAGCTGCTGAAGAGACAATGAACACCAAGCCGGGACTCCTGCCAGCTGCTGAAGAGA 736  
Db 732 CAATGAACACCAGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACGCC 791  
Qy 737 CAATGAACACCAGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACGCC 796  
Db 792 CGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCC 851  
Qy 797 CGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCC 856  
Db 852 CAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCCCTTCTCATTACCTCT 911  
Qy 857 CAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCCCTTCTCATTACCTCT 916  
Db 912 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTGAAAGA 971  
Qy 917 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTGAAAGA 976

Db 972 CTTCACTGTGGAAGAAATTCCCTCCTACCTGAAAGGTTCAGGTAGGCCTGGCTGAGGG 1031  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 977 CTTCACTGTGGAAGAAATTCCCTCCTACCTGAAAGGTTCAGGTAGGCCTGGCTGAGGG 1036

Db 1032 CGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTTGCTGTGTTCCCACAGACAGAAC 1091  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1037 CGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTTGCTGTGTTCCCACAGACAGAAC 1096

Db 1092 GCCTGCCCTGCCCCAA 1108  
||| ||| ||| ||| |||  
Qy 1097 GCCTGCCCTGCCCCAA 1113

RESULT 1: Comparison to SEQ ID NO:2 (Qy)  
 LOCUS AF012536 1180 bp mRNA PRI 21-AUG-1997  
 DEFINITION Homo sapiens decoy receptor 1 (DcR1) mRNA, complete cds.  
 ACCESSION AF012536  
 NID g2338421  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
     Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
     Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
     Homo.  
 REFERENCE 1 (bases 1 to 1180)  
 AUTHORS Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Skubatch,M.,  
     Baldwin,D., Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I.,  
     Goddard,A.D., Godowski,P. and Ashkenazi,A.  
 TITLE Control of TRAIL-induced apoptosis by a family of signaling and  
     decoy receptors  
 JOURNAL Science 277 (5327), 818-821 (1997)  
 MEDLINE 97390509  
 REFERENCE 2 (bases 1 to 1180)  
 AUTHORS Sheridan,J.P., Marsters,S.A., Pitti,R.M., Gurney,A., Baldwin,D.,  
     Ramakrishnan,L., Gray,C.L., Baker,K., Wood,W.I., Goddard,A.D.,  
     Godowski,P. and Ashkenazi,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1997) Molecular Oncology, Genentech, 1 DNA Way,  
     South San Francisco, CA 94080, USA  
 FEATURES Location/Qualifiers  
 source 1. .1180  
     /organism="Homo sapiens"  
     /db\_xref="taxon:9606"  
 gene 1. .1180  
     /gene="DcR1"  
 CDS 193. .972  
     /gene="DcR1"  
     /note="tumor necrosis factor receptor family member;  
     inhibits apoptosis induction by TRAIL/Apo2L"  
     /codon\_start=1  
     /product="decoy receptor 1"  
     /db\_xref="PID:g2338422"  
     /translation="MARIPTKLKVVVIVAVLLPVLAGSATTARQEEVPQQTVAPQQQ  
     RHFSKGEECPAGSHRSEHTGACNPCTEGVDYTNASNEPSCFPCTVCKSDQHKSSCT  
     MTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNTSWDDIQCVEFGANATVE  
     TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPG  
     TPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLIVFV"  
 BASE COUNT 338 a 326 c 298 g 218 t  
 ORIGIN

Query Match 100.0%; Score 1180; DB 22; Length 1180;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 1180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GCTGTGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGA 60  
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 1 GCTGTGGAACCTCTCCACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGA 60

Db 61 GTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTCCTACCGTTAGGAACTCTGGGAC 120  
|||  
Qy 61 GTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTCCTACCGTTAGGAACTCTGGGAC 120

Db 121 AGAGCGCCCCGGCCGCGCTGATGGCGAGGCAGGGTGCACCGACCCAGGACCGACGGCGTC 180  
|||  
Qy 121 AGAGCGCCCCGGCCGCGCTGATGGCGAGGCAGGGTGCACCGACCCAGGACCGACGGCGTC 180

Db 181 GGGAACCATACCATGGCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCG 240  
|||  
Qy 181 GGGAACCATACCATGGCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCG 240

Db 241 GTCCTGCTGCCAGTCCTAGCTTACTCTGCCACACTGCCGGCAGGAGGAAGTTCCCCAG 300  
|||  
Qy 241 GTCCTGCTGCCAGTCCTAGCTTACTCTGCCACACTGCCGGCAGGAGGAAGTTCCCCAG 300

Db 301 CAGACAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGAGGAGTGTCCAGCAGGA 360  
|||  
Qy 301 CAGACAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGAGGAGTGTCCAGCAGGA 360

Db 361 TCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACC 420  
|||  
Qy 361 TCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACC 420

Db 421 AACGCTTCCAACAATGAACCTTCTTGCCTCCCAGTGTACAGTTGTAAATCAGATCAAAAA 480  
|||  
Qy 421 AACGCTTCCAACAATGAACCTTCTTGCCTCCCAGTGTACAGTTGTAAATCAGATCAAAAA 480

Db 481 CATAAAAGTTCTGCACCATGACCAGAGACACAGTGTGTCAAGTGTAAAGAAGGCACCTTC 540  
|||  
Qy 481 CATAAAAGTTCTGCACCATGACCAGAGACACAGTGTGTCAAGTGTAAAGAAGGCACCTTC 540

Db 541 CGGAATGAAAATCCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTC 600  
|||  
Qy 541 CGGAATGAAAATCCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTC 600

Db 601 CAAGTCAGTAATTGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAAT 660  
|||  
Qy 601 CAAGTCAGTAATTGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAAT 660

Db 661 GCCACTGTGGAAACCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCC 720  
|||  
Qy 661 GCCACTGTGGAAACCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCC 720

Db 721 CCAGCTGCTGAAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAG 780  
|||  
Qy 721 CCAGCTGCTGAAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAG 780

Db 781 ACAATGACCACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCGC 840  
|||  
Qy 781 ACAATGACCACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCGC 840

Db 841 CCGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCGCCGGGACTCCTGCC 900  
|||  
Qy 841 CCGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCGCCGGGACTCCTGCC 900

Db 901 TCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCGATT 960  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 901 TCTTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCGATT 960

Db 961 GTGTTTGTGAAAGACTTCACTGTGGAAGAAATTCCCTTACCTGAAAGGTTCAGGT 1020  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 961 GTGTTTGTGAAAGACTTCACTGTGGAAGAAATTCCCTTACCTGAAAGGTTCAGGT 1020

Db 1021 AGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTTGCTGTGT 1080  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1021 AGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTTGCTGTGT 1080

Db 1081 TCCCACAGACAGAAACGCCTGCCCTGCCCAAAAAAAAAAAAAAAA 1140  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1081 TCCCACAGACAGAAACGCCTGCCCTGCCCAAAAAAAAAAAAAAAA 1140

Db 1141 AAAAAAAAAAAAAAAAAAAAAAAA 1180  
||| ||| ||| ||| ||| ||| |||  
Qy 1141 AAAAAAAAAAAAAAAAAAAAAAAA 1180

RESULT 3: Comparison to SEQ ID NO:2 (Qy)  
 LOCUS AF016267 1388 bp mRNA PRI 16-OCT-1997  
 DEFINITION Homo sapiens TRAIL receptor 3 mRNA, complete cds.  
 ACCESSION AF016267  
 NID g2529564  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
     Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
     Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1388)  
 AUTHORS Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and  
     Tschoopp,J.  
 TITLE Characterization of two receptors binding TRAIL  
 JOURNAL FEBS Lett. (1997) In press  
 REFERENCE 2 (bases 1 to 1388)  
 AUTHORS Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and  
     Tschoopp,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-JUL-1997) Institute of Biochemistry, University of  
     Lausanne, Chemin des Boveresses 155, Epalinges, VD 1066,  
     Switzerland  
 FEATURES Location/Qualifiers  
     source 1. .1388  
           /organism="Homo sapiens"  
           /db\_xref="taxon:9606"  
           /dev\_stage="fetal"  
           /tissue\_type="liver and spleen"  
     CDS 188. .967  
           /function="binds cytotoxic ligand TRAIL"  
           /note="DR4 homolog; contains no intracellular domain"  
           /codon\_start=1  
           /product="TRAIL receptor 3"  
           /db\_xref="PID:g2529565"  
           /translation="MARIPTKLKVIVAVLLPVLAGTATTARQEEVPQQTVAPQQQ  
           RHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQHKSSCT  
           MTRDTVCQCKEGTFRNVNSPEMCRKCSRCPGEVQVSNTSWDDIQCVEFGANATVE  
           TPAAEETMNTSPGTPAPAAETMNTSPGTPAPAAEETMTSPGTPAPAAEETMTSPG  
           TPAPAAEETMTSPGTPASSHYLSCTIVGIIVLIVLLIVFV"  
 BASE COUNT 331 a 415 c 368 g 274 t  
 ORIGIN  
 Query Match 92.0%; Score 1086; DB 22; Length 1388;  
 Best Local Similarity 99.7%; Pred. No. 0.00e+00;  
 Matches 1094; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 Db 13 CACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGAGTTGACCAGAGATGC 72  
     |||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 17 CACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGAGTTGACCAGAGATGC 76  
 Db 73 AAGGGGTGAAGGAGCGCTTCTACCGTTAGG-AACTCTGGGACAGAGCGCCCCGGCCGC 131  
     |||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 77 AAGGGGTGAAGGAGCGCTTCTACCGTTAGGAACTCTGGGACAGAGCGCCCCGGCCGC 136  
 Db 132 CTGATGCCGAGGCAGGGTGCAGCCAGGACCCAGGACGGCGTCGGAACCATACCATGG 191

Qy 137 |||||||CTGATGGCGAGGCAGGGTGCACCCAGGACCCAGGACGGACGGCGTCGGAACCATACCATGG 196  
Db 192 CCCGGATCCCCAAGACCCCTAAAGTCGTCGTCACTCGTCGCCAGTCGGTCTGCTGCCAGTCC 251  
|||  
Qy 197 CCCGGATCCCCAAGACCCCTAAAGTCGTCGTCACTCGTCGCCAGTCGGTCTGCTGCCAGTCC 256  
Db 252 TAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTTCCCAGCAGACAGTGGCCCCAC 311  
|||  
Qy 257 TAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTTCCCAGCAGACAGTGGCCCCAC 316  
Db 312 AGCAACAGAGGCACAGCTCAAGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 371  
|||  
Qy 317 AGCAACAGAGGCACAGCTCAAGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 376  
Db 372 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTCCAACAATG 431  
|||  
Qy 377 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTCCAACAATG 436  
Db 432 AACCTTCTTGCTTCCCATGTACAGTTGTAAATCAGATCAAAACATAAAAGTTCTGCA 491  
|||  
Qy 437 AACCTTCTTGCTTCCCATGTACAGTTGTAAATCAGATCAAAACATAAAAGTTCTGCA 496  
Db 492 CCATGACCAGAGACACAGTGTTCAGTGTAAAGAAGGCACCTCCGGAAATGTTAACTCCC 551  
|||  
Qy 497 CCATGACCAGAGACACAGTGTTCAGTGTAAAGAAGGCACCTCCGGAAATGAAAATCCC 556  
Db 552 CAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGGGAAAGTCCAAGTCAGTAATTGTA 611  
|||  
Qy 557 CAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGGGAAAGTCCAAGTCAGTAATTGTA 616  
Db 612 CGTCCTGGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAAACCC 671  
|||  
Qy 617 CGTCCTGGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAAACCC 676  
Db 672 CAGCTGCTGAAGAGACAATGAACACCAAGCCAGCCGGGACTCCTGCCAGCTGCTGAAGAGA 731  
|||  
Qy 677 CAGCTGCTGAAGAGACAATGAACACCAAGCCAGCCGGGACTCCTGCCAGCTGCTGAAGAGA 736  
Db 732 CAATGAACACCAGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACAGCC 791  
|||  
Qy 737 CAATGAACACCAGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACAGCC 796  
Db 792 CGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCC 851  
|||  
Qy 797 CGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCC 856  
Db 852 CAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCCTCTCATTACCTCT 911  
|||  
Qy 857 CAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCCTCTCATTACCTCT 916  
Db 912 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTCTGATTGTGTTGAAAGA 971  
|||  
Qy 917 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTCTGATTGTGTTGAAAGA 976

Db 972 CTTCACTGTGGAAGAAATTCCCTCCTACCTGAAAGGTTCAGGTAGGCCTGGCTGAGGG 1031  
|||  
Qy 977 CTTCACTGTGGAAGAAATTCCCTCCTACCTGAAAGGTTCAGGTAGGCCTGGCTGAGGG 1036

Db 1032 CGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTGCTGTGTTCCCACAGACAGAAC 1091  
|||  
Qy 1037 CGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTGCTGTGTTCCCACAGACAGAAC 1096

Db 1092 GCCTGCCCTGCCCAA 1108  
|||  
Qy 1097 GCCTGCCCTGCCCAA 1113

RESULT 2: Comparison to SEQ ID NO:4 (Qy)  
 LOCUS AF033854 1377 bp mRNA PRI 27-NOV-1997  
 DEFINITION Homo sapiens lymphocyte inhibitor of TRAIL (LIT) mRNA, complete cds.  
 ACCESSION AF033854  
 NID g2645841  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1377)  
 AUTHORS Mongkolsapaya,J., Cowper,A., Xu,X., Morris,G., McMichael,A.J.,  
 Bell,J.I. and Screamton,G.R.  
 TITLE Lymphocyte inhibitor of TRAIL: A new receptor protecting  
 lymphocytes from the death ligand TRAIL  
 JOURNAL J. Immunol. ~~(1997) In press~~ 160(1): 3-6, Jan. 1, 1998  
 REFERENCE 2 (bases 1 to 1377)  
 AUTHORS Mongkolsapaya,J., Cowper,A., Xu,X., Morris,G., McMichael,A.J.,  
 Bell,J.I. and Screamton,G.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-NOV-1997) Immunology, Institute of Molecular  
 Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DS, UK  
 FEATURES Location/Qualifiers  
 source 1..1377  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /cell\_type="lymphocyte"  
 gene 1..1377  
 /gene="LIT"  
 CDS 177..956  
 /gene="LIT"  
 /function="TRAIL receptor"  
 /note="TNF receptor family member; lacks a cytoplasmic  
 domain"  
 /codon\_start=1  
 /product="lymphocyte inhibitor of TRAIL"  
 /db\_xref="PID:g2645842"  
 /translation="MARIPTKLKFVVIVAVLLPVILAYSATTARQEEVPQQTVAPQQC  
 RHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCT  
 MTRDTVCQCKEGTFRNENSPEMCRKCSRCPSPGEVQVSNCSTSDDIQCVEFGANATVE  
 TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPG  
 TPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV"

Query Match 93.0%; Score 1097; DB 22; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 1097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CACGCGCACGAACCTAGCCAACGATTCTGATAGATTTGGAGTTGACCAGAGATGC 60

QY 17 CACCGCGCACGAACCTCAGCCAACGATTCTGATAGATTTGGAGTTGACCAGAGATGC 76

Db 61 AAGGGGTGAAGGAGCGCTTCCACCGTTAGGAACTCTGGGGACAGAGCGCCCCGGCCGC 120

Qy 77 |||||||AAGGGGTGAAGGAGCGCTCCTACCGTTAGGAACCTCTGGGGACAGAGCGCCCCGGCCGC 136  
Db 121 CTGATGGCGAGGCAGGGTGCAGCCAGGACCCAGGACGGCGTCGGAACCATACCATGG 180  
Qy 137 CTGATGGCGAGGCAGGGTGCAGCCAGGACCCAGGACGGCGTCGGAACCATACCATGG 196  
Db 181 CCCGGATCCCCAAGACCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGCCAGTCC 240  
Qy 197 CCCGGATCCCCAAGACCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGCCAGTCC 256  
Db 241 TAGCTTACTCTGCCACCACTGCCCGGAGGAGTTCAGCAGACAGTGGCCCCAC 300  
Qy 257 TAGCTTACTCTGCCACCACTGCCCGGAGGAGTTCAGCAGACAGTGGCCCCAC 316  
Db 301 AGCAACAGAGGCACAGCTCAAGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 360  
Qy 317 AGCAACAGAGGCACAGCTCAAGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 376  
Db 361 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATG 420  
Qy 377 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATG 436  
Db 421 AACCTTCTTGCTTCCCATGTACAGTTGTAAATCAGATCAAAAACATAAAAGTTCTGCA 480  
Qy 437 AACCTTCTTGCTTCCCATGTACAGTTGTAAATCAGATCAAAAACATAAAAGTTCTGCA 496  
Db 481 CCATGACCAGAGACACAGTGTTCAGTGTAAAGAAGGCACCTCCGGAAATGAAAATCCC 540  
Qy 497 CCATGACCAGAGACACAGTGTTCAGTGTAAAGAAGGCACCTCCGGAAATGAAAATCCC 556  
Db 541 CAGAGATGTGCCCGGAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAATTGTA 600  
Qy 557 CAGAGATGTGCCCGGAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAATTGTA 616  
Db 601 CGTCCTGGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAAACCC 660  
Qy 617 CGTCCTGGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAAACCC 676  
Db 661 CAGCTGCTGAAGAGACAATGAACACCAGCCCCGGGACTCCTGCCCTGCCCCAGCTGCTGAAGAGA 720  
Qy 677 CAGCTGCTGAAGAGACAATGAACACCAGCCCCGGGACTCCTGCCCTGCCCCAGCTGCTGAAGAGA 736  
Db 721 CAATGAACACCAGCCCCAGGGACTCCTGCCCTGCCCCAGCTGCTGAAGAGACAATGACCACAGCC 780  
Qy 737 CAATGAACACCAGCCCCAGGGACTCCTGCCCTGCCCCAGCTGCTGAAGAGACAATGACCACAGCC 796  
Db 781 CGGGGACTCCTGCCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAAGCCCCGGGACTCCTGCC 840  
Qy 797 CGGGGACTCCTGCCCTGCCCCAGCTGCTGAAGAGACAATGACCACCAAGCCCCGGGACTCCTGCC 856  
Db 841 CAGCTGCTGAAGAGACAATGACCACCAAGCCCCGGGACTCCTGCCCTTCTCATTACCTCT 900  
Qy 857 CAGCTGCTGAAGAGACAATGACCACCAAGCCCCGGGACTCCTGCCCTTCTCATTACCTCT 916

Db 901 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTGTTGAAAGA 960  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 917 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTGTTGAAAGA 976

Db 961 CTTCACTGTGGAAGAAATTCCCTCCTACCTGAAAGGTTCAGGTAGGCCTGGCTGAGGG 1020  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 977 CTTCACTGTGGAAGAAATTCCCTCCTACCTGAAAGGTTCAGGTAGGCCTGGCTGAGGG 1036

Db 1021 CGGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGACAGAAC 1080  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1037 CGGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGACAGAAC 1096

Db 1081 GCCTGCCCTGCCCAA 1097  
||| ||| ||| |||  
Qy 1097 GCCTGCCCTGCCCAA 1113

RESULT 2: Comparison to SEQ ID NO:2 (Qy)  
 LOCUS AF033854 1377 bp mRNA PRI 27-NOV-1997  
 DEFINITION Homo sapiens lymphocyte inhibitor of TRAIL (LIT) mRNA, complete cds.  
 ACCESSION AF033854  
 NID g2645841  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1377)  
 AUTHORS Mongkolsapaya,J., Cowper,A., Xu,X., Morris,G., McMichael,A.J.,  
 Bell,J.I. and Scream,G.R.  
 TITLE Lymphocyte inhibitor of TRAIL: A new receptor protecting  
 lymphocytes from the death ligand TRAIL  
 JOURNAL J. Immunol. (1997) In press  
 REFERENCE 2 (bases 1 to 1377)  
 AUTHORS Mongkolsapaya,J., Cowper,A., Xu,X., Morris,G., McMichael,A.J.,  
 Bell,J.I. and Scream,G.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-NOV-1997) Immunology, Institute of Molecular  
 Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DS, UK  
 FEATURES Location/Qualifiers  
 source 1. .1377  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /cell\_type="lymphocyte"  
 gene 1. .1377  
 /gene="LIT"  
 CDS 177. .956  
 /gene="LIT"  
 /function="TRAIL receptor"  
 /note="TNF receptor family member; lacks a cytoplasmic  
 domain"  
 /codon\_start=1  
 /product="lymphocyte inhibitor of TRAIL"  
 /db\_xref="PID:g2645842"  
 /translation="MARIPKTLKFVVIVAVLLPVlaysATTARQEEVPQQTVAPQQQ  
 RHFSGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCT  
 MTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCWSDDIQCVEFGANATVE  
 TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTSPGTPAPAAEETMTSPG  
 TPAPAAEETMTSPGTPASSHYLSCTIVGIIVLIVLLIVFV"

BASE COUNT 335 a 409 c 365 g 268 t  
 ORIGIN

Query Match 93.0%; Score 1097; DB 22; Length 1377;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 1097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGAGTTGACCAGAGATGC 60

|||||||||||||||||||||||||||||

Qy 17 CACGCGCACGAACTCAGCCAACGATTCTGATAGATTTGGGAGTTGACCAGAGATGC 76

Db 61 AAGGGGTGAAGGAGCGCTTCCTACCGTTAGGAACTCTGGGACAGAGCGCCCCGGCCGC 120

Qy 77 ||||||| AAGGGTGAAGGAGCGCTTCCCTACCGTAGGAACTCTGGGACAGAGGCCCGGCCGC 136  
Db 121 CTGATGCCGAGGCAGGGTGCAGCCAGGACCCAGGACGGCGTCGGAACCATACCATGG 180  
Qy 137 CTGATGCCGAGGCAGGGTGCAGCCAGGACCCAGGACGGCGTCGGAACCATACCATGG 196  
Db 181 CCCGGATCCCCAAGACCCTAAAGTCGTCGTCACTCGTCGGTCCTGCTGCCAGTCC 240  
Qy 197 CCCGGATCCCCAAGACCCTAAAGTCGTCGTCACTCGTCGGTCCTGCTGCCAGTCC 256  
Db 241 TAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTTCCCAGCAGACAGTGGCCCCAC 300  
Qy 257 TAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTTCCCAGCAGACAGTGGCCCCAC 316  
Db 301 AGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 360  
Qy 317 AGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAAC 376  
Db 361 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATG 420  
Qy 377 ATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAACAATG 436  
Db 421 AACCTTCTGCTTCCATGTACAGTTGAAATCAGATCAAAAACATAAAAGTTCTGCA 480  
Qy 437 AACCTTCTGCTTCCATGTACAGTTGAAATCAGATCAAAAACATAAAAGTTCTGCA 496  
Db 481 CCATGACCAGAGACACAGTGTGTCAGTGAAAGAAGGCACCTCCGGAATGAAAACCTCCC 540  
Qy 497 CCATGACCAGAGACACAGTGTGTCAGTGAAAGAAGGCACCTCCGGAATGAAAACCTCCC 556  
Db 541 CAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAATTGTA 600  
Qy 557 CAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAATTGTA 616  
Db 601 CGTCCTGGATGATATCCAGTGTGTTGAAGAATTGGTCCAATGCCACTGTGGAAACCC 660  
Qy 617 CGTCCTGGATGATATCCAGTGTGTTGAAGAATTGGTCCAATGCCACTGTGGAAACCC 676  
Db 661 CAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGA 720  
Qy 677 CAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGA 736  
Db 721 CAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACAGCC 780  
Qy 737 CAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACAGCC 796  
Db 781 CGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACAGCCGGGACTCCTGCC 840  
Qy 797 CGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACAGCCGGGACTCCTGCC 856  
Db 841 CAGCTGCTGAAGAGACAATGACCACAGCCGGGACTCCTGCCCTTCTCATTACCTCT 900  
Qy 857 CAGCTGCTGAAGAGACAATGACCACAGCCGGGACTCCTGCCCTTCTCATTACCTCT 916

Db 901 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTGAAAGA 960  
|||  
Qy 917 CATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCTGATTGTGTTGAAAGA 976

Db 961 CTTCACTGTGGAAGAAATTCCCTCCTAACCTGAAAGGTTCAGGTAGGCGCTGGCTGAGGG 1020  
|||  
Qy 977 CTTCACTGTGGAAGAAATTCCCTCCTAACCTGAAAGGTTCAGGTAGGCGCTGGCTGAGGG 1036

Db 1021 CGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGACAGAAC 1080  
|||  
Qy 1037 CGGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTCTGCTGTGTTCCCACAGACAGAAC 1096

Db 1081 GCCTGCCCTGCCCAA 1097  
|||  
Qy 1097 GCCTGCCCTGCCCAA 1113

RESULT 4: Comparison to SEQ ID NO:4 (Qy)  
 LOCUS AF014794 1365 bp mRNA PRI 13-MAR-1998  
 DEFINITION Homo sapiens TNF related TRAIL receptor (TRAIL-R3) mRNA, complete  
 cds.  
 ACCESSION AF014794  
 NID g2957263  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1365)  
 AUTHORS Degli-Esposti,M.A., Smolak,P.J., Walczak,H., Waugh,J., Huang,C.P.,  
 DuBose,R.F., Goodwin,R.G. and Smith,C.A.  
 TITLE Cloning and characterization of TRAIL-R3, a novel member of the  
 emerging TRAIL receptor family *oct. 6*  
 JOURNAL J. Exp. Med. 186 (7), 1165-1170 (1997)  
 MEDLINE 97461602  
 REFERENCE 2 (bases 1 to 1365)  
 AUTHORS Degli-Esposti,M.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-JUL-1997) Biochemistry, Immunex, 51 University  
 Street, Seattle, WA 98101, USA  
 FEATURES Location/Qualifiers  
 source 1. .1365  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="8"  
 /map="8p22-p21"  
 gene 1. .1365  
 /gene="TRAIL-R3"  
 CDS 30. .929  
 /gene="TRAIL-R3"  
 /codon\_start=1  
 /product="TNF related TRAIL receptor"  
 /db\_xref="PID:g2957264"  
 /translation="MQGVKERFLPLGNNSDRAAPRPPDGRGRVRPRTQDGVNHTMARI  
 PKTLKFVVIVAVLLPVLAGSATTARQEEVQQTVAPQQQRHSFKGECPAGSHRSEH  
 TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTRDTVCQCKEGTFRNEN  
 SPEMCRKCSRCPSGEVQVSNCTSDDIQCVEEFGANATVETPAAEETMNTSPGTPAPA  
 AEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPA  
 SSHYLSCTIVGIIVLIVLLIVFV"  
 BASE COUNT 332 a 403 c 363 g 267 t  
 ORIGIN

Query Match 89.6%; Score 1057; DB 22; Length 1365;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 1057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 14 GGGAGTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCCTACCGTTAGGAACTCTGG 73  
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 57 GGGAGTTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCCTACCGTTAGGAACTCTGG 116

Db 74 GGACAGAGCGCCCCGGCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACGG 133  
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 117 GGACAGAGCGCCCCGGCCGCTGATGCCGAGGCAGGGTGCACCCAGGACCCAGGACGG 176  
Db 134 CGTCGGGAACCATAACCATGCCCGGATCCCCAAGACCTAAAGTTCGTCGTCACTCGT 193  
|||  
Qy 177 CGTCGGGAACCATAACCATGCCCGGATCCCCAAGACCTAAAGTTCGTCGTCACTCGT 236  
Db 194 CGCGGTCCCTGCTGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGCAGGAGGAAGTTCC 253  
|||  
Qy 237 CGCGGTCCCTGCTGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGCAGGAGGAAGTTCC 296  
Db 254 CCAGCAGACAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGGAGGGAGTGTCCAGC 313  
|||  
Qy 297 CCAGCAGACAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGGAGGGAGTGTCCAGC 356  
Db 314 AGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATT A 373  
|||  
Qy 357 AGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATT A 416  
Db 374 CACCAACGCTTCCAACAATGAACCTTCTGCTTCCCATGTACAGTTGTAAATCAGATCA 433  
|||  
Qy 417 CACCAACGCTTCCAACAATGAACCTTCTGCTTCCCATGTACAGTTGTAAATCAGATCA 476  
Db 434 AAAACATAAAAGTTCTGCACCATGACCAGAGACACAGTGTGTCACTGTAAAGAAGGCAC 493  
|||  
Qy 477 AAAACATAAAAGTTCTGCACCATGACCAGAGACACAGTGTGTCACTGTAAAGAAGGCAC 536  
Db 494 CTTCCGGAATGAAAACCTCCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGA 553  
|||  
Qy 537 CTTCCGGAATGAAAACCTCCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGA 596  
Db 554 AGTCCAAGTCAGTAATTGTACGTCTGGGATGATATCCAGTGTGTGAAGAATTGGTGC 613  
|||  
Qy 597 AGTCCAAGTCAGTAATTGTACGTCTGGGATGATATCCAGTGTGTGAAGAATTGGTGC 656  
Db 614 CAATGCCACTGTGGAAACCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCC 673  
|||  
Qy 657 CAATGCCACTGTGGAAACCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCC 716  
Db 674 TGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGA 733  
|||  
Qy 717 TGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGA 776  
Db 734 AGAGACAATGACCACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCAC 793  
|||  
Qy 777 AGAGACAATGACCACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCAC 836  
Db 794 CAGCCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCC 853  
|||  
Qy 837 CAGCCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCC 896  
Db 854 TGCCTCTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCT 913  
|||  
Qy 897 TGCCTCTCTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCT 956  
Db 914 GATTGTGTTGTTGAAAGACTTCACTGTGGAAGAAATTCCCTCCTACCTGAAAGGTT C 973

Qy 957 ||||||| GATTGTGTTGTTGAAAGACTTCAGTGGAGAAATTCTCCTTACCTGAAAGGTTC 1016  
Db 974 AGGTAGGCCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTGCT 1033  
|||  
Qy 1017 AGGTAGGCCTGGCTGAGGGCGGGGGCGCTGGACACTCTCTGCCCTGCCTCCCTGCT 1076  
Db 1034 GTGTTCCCACAGACAGAAACGCCTGCCCTGCCCAA 1070  
|||  
Qy 1077 GTGTTCCCACAGACAGAAACGCCTGCCCTGCCCAA 1113

RESULT 4: Comparison to SEQ ID NO:2 (Qy)  
 LOCUS AF014794 1365 bp mRNA PRI 13-MAR-1998  
 DEFINITION Homo sapiens TNF related TRAIL receptor (TRAIL-R3) mRNA, complete cds.  
 ACCESSION AF014794  
 NID g2957263  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1365)  
 AUTHORS Degli-Esposti,M.A., Smolak,P.J., Walczak,H., Waugh,J., Huang,C.P.,  
 DuBose,R.F., Goodwin,R.G. and Smith,C.A.  
 TITLE Cloning and characterization of TRAIL-R3, a novel member of the  
 emerging TRAIL receptor family  
 JOURNAL J. Exp. Med. 186 (7), 1165-1170 (1997)  
 MEDLINE 97461602  
 REFERENCE 2 (bases 1 to 1365)  
 AUTHORS Degli-Esposti,M.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-JUL-1997) Biochemistry, Immunex, 51 University  
 Street, Seattle, WA 98101, USA  
 FEATURES Location/Qualifiers  
 source 1. .1365  
     /organism="Homo sapiens"  
     /db\_xref="taxon:9606"  
     /chromosome="8"  
     /map="8p22-p21"  
 gene 1. .1365  
     /gene="TRAIL-R3"  
 CDS 30. .929  
     /gene="TRAIL-R3"  
     /codon\_start=1  
     /product="TNF related TRAIL receptor"  
     /db\_xref="PID:g2957264"  
     /translation="MQGVKERFLPLGNSGDRAPRPPDGRGRVRPRTQDGVGNHTMARI  
     PKTLKFVVIVAVLLPVLAGTATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEH  
     TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHSSCTMTRDTVCQCKEGTFRNEN  
     SPEMCRKCSRCPSPGEVQVSNCTSWSDDIQCVEEFGANATVETPAAEETMNTSPGTPAPA  
     AEETMNTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPA  
     SSHYLSCTIVGIIVLIVLLIVFV"  
 BASE COUNT 332 a 403 c 363 g 267 t  
 ORIGIN

Query Match 89.6%; Score 1057; DB 22; Length 1365;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 1057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 14 GGGAGTTGACCAGAGATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACCTCTGG 73

QY 57 GGGAGTTGACCAAGAGATGCAAGGGGTGAAGGAGCGCTTCTAACCGTTAGGGAACTCTGG 116

Db 74 GGACAGAGCGCCCCGGCCGCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGG 133

Qy 117 GGACAGAGGCCCGGCCCTGATGCCGAGGCAGGGTGCACCCAGGACCCAGGACGG 176  
Db 134 CGTCGGAAACCATAACCATGCCCGGATCCCCAAGACCTAAAGTTCGTCGTACCGT 193  
|||  
Qy 177 CGTCGGAAACCATAACCATGCCCGGATCCCCAAGACCTAAAGTTCGTCGTACCGT 236  
Db 194 CGCGGTCCCTGCTGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGCAGGAGGAAGTTCC 253  
|||  
Qy 237 CGCGGTCCCTGCTGCCAGTCCTAGCTTACTCTGCCACCACTGCCCGCAGGAGGAAGTTCC 296  
Db 254 CCAGCAGACAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGC 313  
|||  
Qy 297 CCAGCAGACAGTGGCCCCACAGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGC 356  
Db 314 AGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCGTGCACAGAGGGTGTGGATT 373  
|||  
Qy 357 AGGATCTCATAGATCAGAACATACTGGAGCCTGTAACCGTGCACAGAGGGTGTGGATT 416  
Db 374 CACCAACGCTTCCAACAATGAACCTTCTGCTTCCCATGTACAGTTGTAAATCAGATCA 433  
|||  
Qy 417 CACCAACGCTTCCAACAATGAACCTTCTGCTTCCCATGTACAGTTGTAAATCAGATCA 476  
Db 434 AAAACATAAAAGTCCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCAC 493  
|||  
Qy 477 AAAACATAAAAGTCCTGCACCATGACCAGAGACACAGTGTGTCAGTGTAAAGAAGGCAC 536  
Db 494 CTTCCGGAATGAAAACCTCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGA 553  
|||  
Qy 537 CTTCCGGAATGAAAACCTCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGA 596  
Db 554 AGTCCAAGTCAGTAATTGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTGC 613  
|||  
Qy 597 AGTCCAAGTCAGTAATTGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTGC 656  
Db 614 CAATGCCACTGTGGAAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCC 673  
|||  
Qy 657 CAATGCCACTGTGGAAACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCC 716  
Db 674 TGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGA 733  
|||  
Qy 717 TGCCCCAGCTGCTGAAGAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGA 776  
Db 734 AGAGACAATGACCACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCAC 793  
|||  
Qy 777 AGAGACAATGACCACCAGCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCAC 836  
Db 794 CAGCCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCC 853  
|||  
Qy 837 CAGCCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCC 896  
Db 854 TGCCTCTTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCT 913  
|||  
Qy 897 TGCCTCTTCATTACCTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTTCT 956  
Db 914 GATTGTGTTGTTGAAAGACTTCACTGTGGAAGAAATTCCCTCCTACCTGAAAGGTTC 973

Qy 957 |||||||GATTGTGTTGTTGAAAGACTTCACTGTGGAAGAAATTCCCTCCTTACCTGAAAGGTTC 1016  
Db 974 AGGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTGCCCTGCCTCCCTTGCT 1033  
Qy 1017 |||||||AGGTAGGCGCTGGCTGAGGGCGGGGGCGCTGGACACTCTGCCCTGCCTCCCTTGCT 1076  
Db 1034 GTGTTCCCACAGACAGAAACGCCTGCCCTGCCCAA 1070  
Qy 1077 |||||||GTGTTCCCACAGACAGAAACGCCTGCCCTGCCCAA 1113

RESULT 5: Comparison to SEQ ID NO:2 (Qy)  
 LOCUS AF020502 900 bp mRNA PRI 28-SEP-1997  
 DEFINITION Homo sapiens cytotoxic TRAIL receptor-3 (TRAIL-R3) mRNA, complete  
 cds.  
 ACCESSION AF020502  
 NID g2443819  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 900)  
 AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T.,  
 Cohen,G.M. and Alnemri,E.S.  
 TITLE Identification and Molecular Cloning of Two Novel Receptors for the  
 Cytotoxic ligand TRAIL  
 JOURNAL ~~J. Biol. Chem.~~ ~~in press~~ Oct. 10, 272(41):25417-20,  
 REFERENCE 2 (bases 1 to 900)  
 AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T.,  
 Cohen,G.M. and Alnemri,E.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-AUG-1997) Department of Microbiology and Immunology,  
 Kimmel Cancer Institute, 233 S. 10th Street, Philadelphia, PA  
 19107, USA  
 FEATURES Location/Qualifiers  
 source 1. .900  
       /organism="Homo sapiens"  
       /db\_xref="taxon:9606"  
       /cell\_type="T-lymphocyte"  
       /note="Jurkat"  
 gene 1. .900  
       /gene="TRAIL-R3"  
 CDS 1. .900  
       /gene="TRAIL-R3"  
       /note="TNFR family member; binds cytotoxic ligand TRAIL;  
       antagonistic decoy receptor, does not contain death  
       domain"  
       /codon\_start=1  
       /product="cytotoxic TRAIL receptor-3"  
       /db\_xref="PID:g2443820"  
       /translation="MQGVKERFLPLGNSGDRAPRPPDGRGRVRPRTQDGVGNHTMARI  
       PKTLKFVVIVAVLLPVLAGSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEH  
       TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSCTMTRDTVCQCKEGTFRNEN  
       SPEMCRKCSRCPSPGEVQVSNCWSDDIQCVEFGANATVETPAAEETMNTSPGTTPA  
       AEETMNTSPGTTPAPAAEETMTTSPGTTPAPAAEETMTTSPGTTPAPAAEETMTTSPGTTPA  
       SSHYLSTCIVGIIVLIVLLIVFV"  
 BASE COUNT 228 a 262 c 240 g 170 t  
 ORIGIN  
 Query Match 76.1%; Score 898; DB 22; Length 900;  
 Best Local Similarity 99.9%; Pred. No. 2.87e-262;  
 Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 1 ATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGAACTCTGGGGACAGAGCGCCCCGG 60  
 Qy 73 ATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGAACTCTGGGGACAGAGCGCCCCGG 132

Db 61 CCGCCTGATGGCCGAGGCAGGGTGCACCCAGGACCAAGACGGCGTCGGAACCATACC 120  
|||  
Qy 133 CCGCCTGATGGCCGAGGCAGGGTGCACCCAGGACCAAGACGGCGTCGGAACCATACC 192

Db 121 ATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGCCA 180  
|||  
Qy 193 ATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGCCA 252

Db 181 GTCCTAGCTTACTCTGCCACCACTGCCCGGAGGAGGAAGTTCCCAGCAGACAGTGGCC 240  
|||  
Qy 253 GTCCTAGCTTACTCTGCCACCACTGCCCGGAGGAGGAAGTTCCCAGCAGACAGTGGCC 312

Db 241 CCACAGCAACAGAGGCACAGCTTAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 300  
|||  
Qy 313 CCACAGCAACAGAGGCACAGCTTAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 372

Db 301 GAACATACTGGAGCCTGTAACCGTGACAGAGGGTGTGGATTACACCAACGCTTCCAAC 360  
|||  
Qy 373 GAACATACTGGAGCCTGTAACCGTGACAGAGGGTGTGGATTACACCAACGCTTCCAAC 432

Db 361 AATGAACCTTCTTGCTTCCATGTACAGTTGTAAATCAGATCAAAAACATAAAAGTTCC 420  
|||  
Qy 433 AATGAACCTTCTTGCTTCCATGTACAGTTGTAAATCAGATCAAAAACATAAAAGTTCC 492

Db 421 TGCACCATGACCAGAGACACAGTGTCAAGTGTAAAGAAGGCACCTCCGGATGAAAAC 480  
|||  
Qy 493 TGCACCATGACCAGAGACACAGTGTCAAGTGTAAAGAAGGCACCTCCGGATGAAAAC 552

Db 481 TCCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAAT 540  
|||  
Qy 553 TCCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAAT 612

Db 541 TGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTCCAATGCCACTGTGGAA 600  
|||  
Qy 613 TGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTCCAATGCCACTGTGGAA 672

Db 601 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTGAA 660  
|||  
Qy 673 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTGAA 732

Db 661 GAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACC 720  
|||  
Qy 733 GAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACC 792

Db 721 AGCCCGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCT 780  
|||  
Qy 793 AGCCCGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCT 852

Db 781 GCCCCAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCCCTTCTCATTAC 840  
|||  
Qy 853 GCCCCAGCTGCTGAAGAGACAATGACCACCAAGCCGGGACTCCTGCCCTTCTCATTAC 912

Db 841 CTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTCTGATTGTGTTGTTGA 900  
|||  
Qy 913 CTCTCATGCACCATCGTAGGGATCATAGTTCTAATTGTGCTCTGATTGTGTTGTTGA 972

RESULT 5: Comparison to SEQ ID NO:4 (Qy)  
 LOCUS AF020502 900 bp mRNA PRI 28-SEP-1997  
 DEFINITION Homo sapiens cytotoxic TRAIL receptor-3 (TRAIL-R3) mRNA, complete cds.  
 ACCESSION AF020502  
 NID g2443819  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 900)  
 AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T.,  
 Cohen,G.M. and Alnemri,E.S.  
 TITLE Identification and Molecular Cloning of Two Novel Receptors for the  
 Cytotoxic ligand TRAIL  
 JOURNAL J. Biol. Chem. (1997) In press  
 REFERENCE 2 (bases 1 to 900)  
 AUTHORS MacFarlane,M., Ahmad,M., Srinivasula,S.M., Fernandes-Alnemri,T.,  
 Cohen,G.M. and Alnemri,E.S.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-AUG-1997) Department of Microbiology and Immunology,  
 Kimmel Cancer Institute, 233 S. 10th Street, Philadelphia, PA  
 19107, USA  
 FEATURES Location/Qualifiers  
 source 1..900  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /cell\_type="T-lymphocyte"  
 /note="Jurkat"  
 gene 1..900  
 /gene="TRAIL-R3"  
 CDS 1..900  
 /gene="TRAIL-R3"  
 /note="TNFR family member; binds cytotoxic ligand TRAIL;  
 antagonistic decoy receptor, does not contain death  
 domain"  
 /codon\_start=1  
 /product="cytotoxic TRAIL receptor-3"  
 /db\_xref="PID:g2443820"  
 /translation="MQGVKERFLPLGNSGDRAPRPPDGRGRVRPRTQDGVNHTMARI  
 PKTLKFVVIVAVLLPVILAYSATTARQEEVPQQTVAPQQQRHSFKGEECPAGSHRSEH  
 TGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHKSSCTMTRDTVCQCKEGTFRNEN  
 SPEMCRKCSRCPSGEVQVSNTSWDDIQCVEFGANATVETPAAEETMNTSPGTPAPA  
 AEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPA  
 SSHYLSCTIVGIIVLIVLLIVFV"  
 BASE COUNT 228 a 262 c 240 g 170 t  
 ORIGIN  
 Query Match 76.1%; Score 898; DB 22; Length 900;  
 Best Local Similarity 99.9%; Pred. No. 2.87e-262;  
 Matches 899; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Db 1 ATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGAACTCTGGGGACAGAGCGCCCCGG 60  
 |||||||  
 Qy 73 ATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGAACTCTGGGGACAGAGCGCCCCGG 132

Db 61 CCGCCTGATGGCCGAGGCAGGGTGCACCCAGGACCCAAGACGGCGTCGGGAACCATAAC 120  
|||  
Qy 133 CCGCCTGATGGCCGAGGCAGGGTGCACCCAGGACCCAAGACGGCGTCGGGAACCATAAC 192

Db 121 ATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGCCA 180  
|||  
Qy 193 ATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCGGTCTGCTGCCA 252

Db 181 GTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCAGCAGACAGTGGCC 240  
|||  
Qy 253 GTCCTAGCTTACTCTGCCACCACTGCCCGGCAGGAGGAAGTTCCCAGCAGACAGTGGCC 312

Db 241 CCACAGCAACAGAGGCACAGCTTAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 300  
|||  
Qy 313 CCACAGCAACAGAGGCACAGCTTAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 372

Db 301 GAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAAC 360  
|||  
Qy 373 GAACATACTGGAGCCTGTAACCCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAAC 432

Db 361 AATGAACCTTCTTGCTTCCATGTACAGTTGTAAATCAGATCAAAAACATAAAAGTTCC 420  
|||  
Qy 433 AATGAACCTTCTTGCTTCCATGTACAGTTGTAAATCAGATCAAAAACATAAAAGTTCC 492

Db 421 TGCACCATGACCAGAGACACAGTGTTCAGTGTAAAGAAGGCACCTCCGGATGAAAAC 480  
|||  
Qy 493 TGCACCATGACCAGAGACACAGTGTTCAGTGTAAAGAAGGCACCTCCGGATGAAAAC 552

Db 481 TCCCCAGAGATGTGCCGGAAAGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAAT 540  
|||  
Qy 553 TCCCCAGAGATGTGCCGGAAAGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAAT 612

Db 541 TGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAA 600  
|||  
Qy 613 TGTACGTCTGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAA 672

Db 601 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTGAA 660  
|||  
Qy 673 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTGAA 732

Db 661 GAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACC 720  
|||  
Qy 733 GAGACAATGAACACCAGCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACC 792

Db 721 AGCCCGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCT 780  
|||  
Qy 793 AGCCCGGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCT 852

Db 781 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCTGCCCTTCTCATTAC 840  
|||  
Qy 853 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCTGCCCTTCTCATTAC 912

Db 841 CTCTCATGCACCACGTAGGGATCATAGTTCTAATTGTGTTCTGATTGTGTTGTTGA 900  
|||  
Qy 913 CTCTCATGCACCACGTAGGGATCATAGTTCTAATTGTGTTCTGATTGTGTTGTTGA 972

RESULT 1: Comparison to SEQ ID NO:1 (Qy)

ID O14798 PRELIMINARY; PRT; 299 AA.

AC O14798;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)

DE CYTOTOXIC TRAIL RECEPTOR-3.

GN TRAIL-R3.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RA MACFARLANE M., AHMAD M., SRINIVASULA S.M., FERNANDES-ALNEMRI T.,

RA COHEN G.M., ALNEMRI E.S.;

RL J. BIOL. CHEM. 0:0-0(1997).

DR EMBL; AF020502; G2443820; -.

SQ SEQUENCE 299 AA; 31759 MW; 59B93A14 CRC32;

Query Match 100.0%; Score 1783; DB 2; Length 299;  
Best Local Similarity 100.0%; Pred. No. 5.99e-239;  
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 41 MARIPKTLKFVVVIVAVLLPVlaysATTARQEEVPQQTVAPQQQRHSFKGECPAGSHRS 100  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 1 MARIPKTLKFVVVIVAVLLPVlaysATTARQEEVPQQTVAPQQQRHSFKGECPAGSHRS 60

Db 101 EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHSSCTMTRDTCQCKEGTFRNEN 160  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 61 EHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQKHSSCTMTRDTCQCKEGTFRNEN 120

Db 161 SPEMCRKCSRCPSGEVQSNCTS WDDIQCVEFGANATVETPAAEETMNTSPGT PAPAAE 220  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 121 SPEMCRKCSRCPSGEVQSNCTS WDDIQCVEFGANATVETPAAEETMNTSPGT PAPAAE 180

Db 221 ETMNTSPGT PAPAAEETMTSPGT PAPAAEETMTSPGT PAPAAEETMTSPGT PASSHY 280  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
Qy 181 ETMNTSPGT PAPAAEETMTSPGT PAPAAEETMTSPGT PAPAAEETMTSPGT PASSHY 240

Db 281 LSCTIVGIIVLIVLLIVFV 299  
||| ||| ||| ||| ||| |||  
Qy 241 LSCTIVGIIVLIVLLIVFV 259

RESULT 6: Comparison to SEQ ID NO:2 (Qy)  
 LOCUS AF012629 780 bp mRNA PRI 21-AUG-1997  
 DEFINITION Homo sapiens antagonist decoy receptor for TRAIL/Apo-2L (TRID)  
 mRNA, complete cds.  
 ACCESSION AF012629  
 NID g2338430  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
 Homo.  
 REFERENCE 1 (bases 1 to 780)  
 AUTHORS Pan,G., Ni,J., Wei,Y.F., Yu,G., Gentz,R. and Dixit,V.M.  
 TITLE An antagonist decoy receptor and a death domain-containing receptor  
 for TRAIL Aug. 8  
 JOURNAL Science 277 (5327), 815-818 (1997)  
 MEDLINE 97390508  
 REFERENCE 2 (bases 1 to 780)  
 AUTHORS Pan,G., Ni,J., Wei,Y., Yu,G., Gentz,R. and Dixit,V.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1997) Pathology, University of Michigan, 1301  
 Catherine Road, Room 7518, Ann Arbor, MI 48109, USA  
 FEATURES Location/Qualifiers  
 source 1..780  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 gene 1..780  
 /gene="TRID"  
 CDS 1..780  
 /gene="TRID"  
 /codon\_start=1  
 /product="antagonist decoy receptor for TRAIL/Apo-2L"  
 /db\_xref="PID:g2338431"  
 /translation="MARIPKTLKFVVVIVAVLLPVLAGSATTARQEEVPQQTVAPQQQ  
 RHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQHKSSCT  
 MTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTS WDDIQCVEFGANATVE  
 TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPG  
 TPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV"  
 BASE COUNT 202 a 226 c 196 g 156 t  
 ORIGIN

Query Match 66.1%; Score 780; DB 22; Length 780;  
 Best Local Similarity 100.0%; Pred. No. 2.44e-225;  
 Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1 ATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCCGCTGCTGCCA	60
Qy	193 ATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCCGCTGCTGCCA	252
Db	61 GTCCTAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTCCCCAGCAGACAGTGGCC	120
Qy	253 GTCCTAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTCCCCAGCAGACAGTGGCC	312
Db	121 CCACAGAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA	180

Qy 313 ||||||| CCACAGCAACAGAGGCACAGCTTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 372  
Db 181 GAACATACTGGAGCCTGTAACCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAAC 240  
Qy 373 GAACATACTGGAGCCTGTAACCGTGCACAGAGGGTGTGGATTACACCAACGCTTCCAAC 432  
Db 241 AATGAACCTTCTTGCTTCCCATGTACAGTTGTAAATCAGATCAAAACATAAAAGTTCC 300  
Qy 433 AATGAACCTTCTTGCTTCCCATGTACAGTTGTAAATCAGATCAAAACATAAAAGTTCC 492  
Db 301 TGCACCAGTACAGAGACACAGTGTTCAGTGTAAAGAAGGCACCTCCGAATGAAAAC 360  
Qy 493 TGCACCAGTACAGAGACACAGTGTTCAGTGTAAAGAAGGCACCTCCGAATGAAAAC 552  
Db 361 TCCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGGAAAGTCCAAGTCAGTAAT 420  
Qy 553 TCCCCAGAGATGTGCCGGAAAGTGTAGCAGGTGCCCTAGTGGGGAAAGTCCAAGTCAGTAAT 612  
Db 421 TGTACGTCTGGGATGATATCCAGTGTGTTGAAGAATTGGTCCAATGCCACTGTGGAA 480  
Qy 613 TGTACGTCTGGGATGATATCCAGTGTGTTGAAGAATTGGTCCAATGCCACTGTGGAA 672  
Db 481 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTGAA 540  
Qy 673 ACCCCAGCTGCTGAAGAGACAATGAACACCAGCCGGGACTCCTGCCAGCTGCTGAA 732  
Db 541 GAGACAATGAACACCAGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACC 600  
Qy 733 GAGACAATGAACACCAGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACC 792  
Db 601 AGCCCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCT 660  
Qy 793 AGCCCCGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCT 852  
Db 661 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCTGCCCTTCTCATTAC 720  
Qy 853 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCGGGACTCCTGCCCTTCTCATTAC 912  
Db 721 CTCTCATGCACCACCGTAGGGATCATAGTTCTAATTGTGCTCTGATTGTGTTGTTGA 780  
Qy 913 CTCTCATGCACCACCGTAGGGATCATAGTTCTAATTGTGCTCTGATTGTGTTGTTGA 972

RESULT 6: Comparison to SEQ ID NO:4 (Qy)  
 LOCUS AF012629 780 bp mRNA PRI 21-AUG-1997  
 DEFINITION Homo sapiens antagonist decoy receptor for TRAIL/Apo-2L (TRID)  
 mRNA, complete cds.  
 ACCESSION AF012629  
 NID g2338430  
 KEYWORDS .  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;  
 Homo.  
 REFERENCE 1 (bases 1 to 780)  
 AUTHORS Pan,G., Ni,J., Wei,Y.F., Yu,G., Gentz,R. and Dixit,V.M.  
 TITLE An antagonist decoy receptor and a death domain-containing receptor  
 for TRAIL  
 JOURNAL Science 277 (5327), 815-818 (1997)  
 MEDLINE 97390508  
 REFERENCE 2 (bases 1 to 780)  
 AUTHORS Pan,G., Ni,J., Wei,Y., Yu,G., Gentz,R. and Dixit,V.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-JUL-1997) Pathology, University of Michigan, 1301  
 Catherine Road, Room 7518, Ann Arbor, MI 48109, USA  
 FEATURES Location/Qualifiers  
 source 1. .780  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 gene 1. .780  
 /gene="TRID"  
 CDS 1. .780  
 /gene="TRID"  
 /codon\_start=1  
 /product="antagonist decoy receptor for TRAIL/Apo-2L"  
 /db\_xref="PID:g2338431"  
 /translation="MARIPKTLKFVVVIVAVLLPVLAGSATTARQEEVPQQTVAPQQQ  
 RHSFKGEECPAGSHRSEHTGACNPCTEGVDYTNASNNEPSCFPCTVCKSDQHKSSCT  
 MTRDTVCQCKEGTFRNENSPEMCRKCSRCPSGEVQVSNCTS WDDIQCVEFGANATVE  
 TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPG  
 TPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV"  
 BASE COUNT 202 a 226 c 196 g 156 t  
 ORIGIN  
 Query Match 66.1%; Score 780; DB 22; Length 780;  
 Best Local Similarity 100.0%; Pred. No. 2.44e-225;  
 Matches 780; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 ATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCCGCCTGCTGCCA 60  
 |||||  
 Qy 193 ATGGCCCGGATCCCCAAGACCCCTAAAGTTCGTCGTCATCGTCGCCGCCTGCTGCCA 252  
 |||||  
 Db 61 GTCCTAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTTCCCAGCAGACAGTGGCC 120  
 |||||  
 Qy 253 GTCCTAGCTTACTCTGCCACCACTGCCGGCAGGAGGAAGTTCCCAGCAGACAGTGGCC 312  
 |||||  
 Db 121 CCACAGCAACAGAGGCACAGCTCAAGGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 180

Qy 313 ||||||| CCACAGCAACAGAGGCACAGCTTCAAGGGGAGGAGTGTCCAGCAGGATCTCATAGATCA 372  
Db 181 GAACATACTGGAGCCTGTAACCGTGACAGAGGGTGTGGATTACACCAACGCTTCCAAC 240  
Qy 373 GAACATACTGGAGCCTGTAACCGTGACAGAGGGTGTGGATTACACCAACGCTTCCAAC 432  
Db 241 AATGAACCTTCTTGCCTCCCAGTACAGTTGAAATCAGATCAAAAACATAAAAGTTCC 300  
Qy 433 AATGAACCTTCTTGCCTCCCAGTACAGTTGAAATCAGATCAAAAACATAAAAGTTCC 492  
Db 301 TGCACCAGTACAGAGACACAGTGTGTCACTGTAAAGAAGGCACCTCCGAATGAAAAC 360  
Qy 493 TGCACCAGTACAGAGACACAGTGTGTCACTGTAAAGAAGGCACCTCCGAATGAAAAC 552  
Db 361 TCCCCAGAGATGTGCCGAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAAT 420  
Qy 553 TCCCCAGAGATGTGCCGAAGTGTAGCAGGTGCCCTAGTGGGAAGTCCAAGTCAGTAAT 612  
Db 421 TGTACGTCCTGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAA 480  
Qy 613 TGTACGTCCTGGATGATATCCAGTGTGTTGAAGAATTGGTGCCAATGCCACTGTGGAA 672  
Db 481 ACCCCAGCTGCTGAAGAGACAATGAACACCAAGCCCCGGGACTCCTGCCAGCTGCTGAA 540  
Qy 673 ACCCCAGCTGCTGAAGAGACAATGAACACCAAGCCCCGGGACTCCTGCCAGCTGCTGAA 732  
Db 541 GAGACAATGAACACCAAGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACC 600  
Qy 733 GAGACAATGAACACCAAGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACC 792  
Db 601 AGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGACTCCT 660  
Qy 793 AGCCCAGGGACTCCTGCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGACTCCT 852  
Db 661 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGACTCCTGCCCTTCTCATTAC 720  
Qy 853 GCCCCAGCTGCTGAAGAGACAATGACCACCAGCCCCGGGACTCCTGCCCTTCTCATTAC 912  
Db 721 CTCTCATGCACCACCGTAGGGATCATAGTTCTAATTGTGCTCTGATTGTGTTGTTGA 780  
Qy 913 CTCTCATGCACCACCGTAGGGATCATAGTTCTAATTGTGCTCTGATTGTGTTGTTGA 972